



Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy

Search for
 ☐ 1: CAD58967. Disease resistanc...[gi:26986180]

BLink, Domains, Links

LOCUS CAD58967 318 aa linear PLN 15-DEC-2002
DEFINITION Disease resistance protein NBS-LRR type [Musa acuminata].

ACCESSION CAD58967

VERSION CAD58967.1 GI:26986180

DBSOURCE embl locus MAC534312, accession AJ534312.1

KEYWORDS

SOURCE Musa acuminata

ORGANISM Musa acuminata

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
Musa.

REFERENCE 1 (residues 1 to 318)

AUTHORS Arango, R., Rodriguez, E. and May, G.D.

TITLE Partial cloning of a disease resistance gene analog from Musa
acuminata (Var. Grand Nain)

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 318)

AUTHORS Arango, R.

TITLE Direct Submission

JOURNAL Submitted (08-DEC-2002) Grupo de Biotecnologia Vegetal UNALMED-CIB,
Carrera 72 A No. 78B- 141, Medellin, Antioquia, COLOMBIA

FEATURES

Location/Qualifiers

source

1..318

/organism="Musa acuminata"

/cultivar="Grand Nain"

/db_xref="taxon:4641"

Protein

1..318

/product="Disease resistance protein NBS-LRR type"

Region

137..>304

/region_name="NB-ARC domain"

/note="NB-ARC"

/db_xref="CDD:24492"

CDS

1..318

/gene="disease resistance NBS-LRR type gene"

/coded_by="AJ534312.1:<1..957"

/db_xref="GOA:Q8GUB6"

/db_xref="UniProt/TrEMBL:Q8GUB6"

ORIGIN

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1  vhdeiketlt  acfqlrrtrn sltealsdlr ataqrvkdkv eeeeahqric npdvrrwqkk
61  vdeilrecda  ggeheepkrc acfcgcdmdl lhrhrvarkv vqnlqdvnlk ksdgdaftpp
121 fnhepppepv eelpfetqti gmelalsqll srfdeaeksi igvhlgggvg ktlllktltn
181 elkentrdyh vvimievans etlnvvdmgk iianrlalpW neseterers tylrralrrk
241 kfvllldvW kkfqladvgi ptpssdkgck lilasrsnqv cvemgdkepm empclgdnes
301 lrlfpeqldg rgqcrhrp
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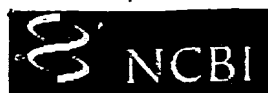
//

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Oct 4 2004 14:35:49

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Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ Align

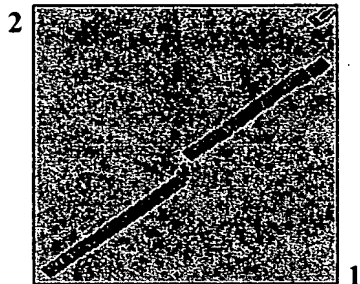
Prior art

claimed

Sequence 1 lcl|seq_1 Length 918 (1 .. 918)

Sequence 2 lcl|seq_2 Length 1232 (1 .. 1232)

D1 SEQ ID NO: 42 x SEQ ID NO: 4



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 389 bits (999), Expect = e-106

Identities = 303/949 (31%), Positives = 448/949 (46%), Gaps = 139/949 (14%)

Query: 42 AVLEDAQEKQLNDKPLENLWLQKLNAATYEVDDILDEYKTKATRF--LQSEYGRYHPKVI- 98
++LE+A+ +++ DK L WL +L Y+ DDILDEY+ A R +S + R VI
Sbjct: 52 SLLEEAKARRMTDKSLVLWLMELKEWAYDADDILDEYEA A IRLKVTRSTFKRLIDHVII 111

Query: 99 --PFRHKVKGKRMQVMKKLNAIAEERK-NFHLQEKI IERQAATRE-TGSVLTEPQVYGRD 154
P HKV + K+LN + ER+ N E + R T S+LTE + GR
Sbjct: 112 NVPLAHKVA----DIRKRLNGVTLERELNLGALEGSQPLDSTKRGVTTSLLTESCIVGRA 167

Query: 155 KEKDEIVKILINNVSDAQKLSVLPLMGGLGKTTLSQMVFNDQRVTERFYPKIWIWCVSD 214
++K+ +++L+ A + V+PI+G+GG GKTTLSQ++FND+RV E F ++W+CVSD
Sbjct: 168 QDKENLIRLLLEPSDGA--VPVPIVGLGGAGKTTLSQLIFNDKRVEEHFPLRMWVCVSD 225

Query: 215 DFDEKRLIKAIVE-SIEGKSLSDMDLAPLQKKLQELLNGKRYFLVLDDVWVNEDQHKWANL 273
DFD KR+ + I E + G+ + +L LQ L+E + G + LVLDDVWVNED KW +L
Sbjct: 226 DFDVKRITREITEYATNGRFMDLTNLNMLQVNLKKEIRGTTFLVLDDVWVNEDPVKWESL 285

Query: 274 RAVLKVGASGAFVLTTRLEKVGSI MGTLQPYELSNLSPEDCWFLFMQRAFGHQ--EEIN 331
A L G G+ V+ TT+ +KV + GT++PY L L+ +D W L +F N
Sbjct: 286 LAPLDAGGRGSVVIVTTQSKKVADVTGTMEPYVLEELTEDDSWSLIESHSFREASCSSTN 345

Query: 332 PNLVAIGKEIVKCGGVPLAAKTGGILRFKREEREWEHV-DSPIWNLPQDESSILPALR 390
P + IG++I KK G+P A +G LR K E W V ++ W +P S +L ALR
Sbjct: 346 PRMEEIGRKIAKKISGLPYGATAMGRYLRSKHGESSWREVLETETWEMPPAASDVLSALR 405

Query: 391 LSYHHLPLDLQCFVYCAVFPKDTKMAKENLIAFWMAHGFLLSKGNLELEDV----- 442
SY +LP L CF +CA+F K + K+ LI W+A + S + ED+
Sbjct: 406 RSYDNLPPQLKLCFAFCALFTKGYRFRKDTLIHMWIAQNLIQSTESKRSEDMAEECFDDL 465

Query: 443 -----NEVWNEL-----YLRVSSYSPSLLQK----- 463
N V N+ Y R SP + K
Sbjct: 466 VCRFFFRYSWGNVVMNDSVHDLARWVSLDEYFRAEDSPLHISKPIRHLWCSEITNVL 525

Query: 464 -----FXXXXXXXXXXXXXQLPSSI 484
LPSS+

Sbjct: 526 EDNNTGGDAVNPLSSLRTLLFLGQSEFRSYHLLDRMFRMLSRIRVLDFSNCVIRNLPSSV 585

Query: 485 GDLVHLRYLDLSGNFRIRNLPKRLCKLQNLQTLDLHYCDSLSCLPKQTSKLGSLRNLLD 544
G+L HLRYL LS N RI+ LP+ + +L LQTL L C+ L LP+ S+L LR L +

Sbjct: 586 GNLKHLRYLGLS-NTRIQRLPESVTRLCLLQTLLEGE-LCRLPRSMSRLVKLRQLKAN 643

Query: 545 GCSLTSTPPRIGLLTCLKSLSCFVIGKRKGQYLGELKNLN-LYGSISITKLDREVKKSDA 603
+ + ++G L L+ L + + K+KG+ + EL +N L+G +SI L V+K ++

Sbjct: 644 P-DVIADIAKVGRLIELQELKAYNVDKKKGHGIAELSAMNQLHGDLSIRNLQNVEKTRES 702

Query: 604 KEANLSAKANLHSLCLSWDLGDKHR----YDSEVLEALKPHSNLKYLEINGFGGIRLPDW 659
++A L K L L L W DG+ D +VL+ L+PH NL+ L I +GG P W

Sbjct: 703 RKARLDEKQKLKLLDLRW-ADGRGAGECDRDRKVLKGLRPHPNLRELSIKYYGGTSSPSW 761

Query: 660 MNQSVLKNVVSIRIRGCENCSCLPFFGELPCLESLELHTGSADVEYVEDNVH----PGRF 715
M L N+ +IR+R C + LP G+L L L + G + V + + F

Sbjct: 762 MTDQYLPNMETIRLRSCARLTCLGQLHLRHLHI-DGMSQVRQINLQFYGTGEVSGF 820

Query: 716 PSLRKLVIWDFSNLKGLLK-KEGEEQFPVLEEMTFYWCP-MFVIPTLSSVKTCLKVIATDA 773
P L L I +L+ + + FP L ++ CP + +P+L TL+ +

Sbjct: 821 PLELLNIRRMPSLEEWSEPRRNCCYFPRHLKLLIEDCPRLRNLPSP--PTLEELRISR 878

Query: 774 TVLRSISNLRALTSLDISNNVEATSLPEEMFKSLANLKYLNISFFRNKELPTXXXXXXX 833
T L + + D++ NV +SL + L +L + NL L T

Sbjct: 879 TGLVDLPGFHG--NGDVTTNVSLSLHVSECRELRSLSEGLLQ--HNLVALKT----- 927

Query: 834 XXXXXFEFCNALESPLAEGVKGLTSLTELSVSNMMLKC---LPEGLQH 879
F C++LE LPAEG + SL L ++NC L C LP L+H

Sbjct: 928 ---AAFTDCDSLEFLPAEGFRTAISLESIMTNC-PLPCSFLLPSSLEH 972

Score = 43.9 bits (102), Expect = 0.036

Identities = 24/75 (32%), Positives = 37/75 (49%), Gaps = 1/75 (1%)

Query: 842 CNALESPLAEGVKGLTSLTELSVSNMMLKCLPEGLQHXXXXXXXXXXQCPIVFKRCERGI 901
C LE LPA ++ L SL+ L + C + P G +CP + +RC+

Sbjct: 1148 CPNLEVL PAN-LQSLCSLSTLYIVRCPRIHAFFPGVSM SLAHLVIHECPQLCQRCDPPG 1206

Query: 902 GEDWHKIAHIPYLT 916
G+DW IA++P + L

Sbjct: 1207 GDDWPLIANVPRICL 1221

CPU time: 0.16 user secs. 0.00 sys. secs 0.16 total secs.

Lambda K H
0.320 0.137 0.410

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 7820

Number of extensions: 5118

Number of successful extensions: 24

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's gapped: 7

Number of HSP's successfully gapped: 2

Number of extra gapped extensions for HSPs above 10.0: 0

Length of query: 918

Length of database: 765,028,816

Length adjustment: 140

Effective length of query: 778

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<http://www.mobi-nlms.nih.gov/blast/blast2.cgi?seq=20>



Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ Align

Prior art

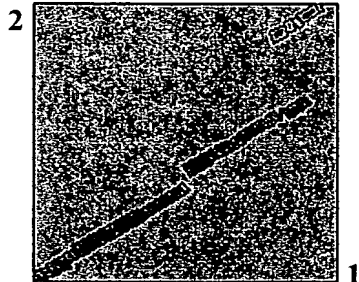
claimant

Sequence 1 lcl|seq_1 Length 918 (1 .. 918)

D1

SEQ ID NO: 42 x SEQ ID NO: 2

Sequence 2 lcl|seq_2 Length 1441 (1 .. 1441)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 375 bits (964), Expect = e-102

Identities = 286/950 (30%), Positives = 437/950 (45%), Gaps = 155/950 (16%)

```

Query: 2  AEAFIQVVLDNLTSLFKGELVLLFGFQDEFQ-LSSMFSTIQAVLEDAQEK-QLNDKPLEN 59
      A++FIQ +LD ++      +L   G  D+ + L +   I A+L+ A+ +   + L
Sbjct: 12  AQSFIQTLLDKASNCAIQQLARRRGLHDDLRLRLRTSLLRIHAILDKAETRWNHKNTSLVE 71

Query: 60  WLQKLNAATYEVDLDILDEYKTKATRFLOSEYGRYHPKVIPFR-----HKVGKR 107
      +++L  A Y+ +D+L+E + +A +   G      + F           G R
Sbjct: 72  LVRQLKDAAYDAEDLLEELEYQAAKQKVEHRGDQISDLFSFSLSTASEWLGAAGDDAGTR 131

Query: 108  MDQVMKKLNIAIEERKNFHLQ-----EKIIERQAATRETGSVLTEPQVYGRDKEKDEIV 161
      + ++ KL  IA +   +   + + +   RET S LTE  V+GRD+E+++V
Sbjct: 132  LREIQGKLCNIAADMMDVMQLLAPDDGGRQFDWKVVRRETSSFLTETVVFGRDQEREKVV 191

Query: 162  KILINNVSDAQKLSVLPILGMGGLGKTTLSQMVFNQDQVTERFYPKIWIICVSDDFDEKRL 221
      ++L+++ S      SVLP++G+GG+GKTTL+Q+V+ND RV   F+ K+W+CVSD+F+ KRL
Sbjct: 192  ELLLDGSGSGNSSFSVLPLVGIGGVGKTTLAQLVYNDNRVGNFYHLKVWVCVSDNFNVKRL 251

Query: 222  IKAIVESIEGKSLSD-MDLAPLQKKLQELLNGKRYFLVLDDVWVEDQHKWANLRAVLKVG 280
      K I+ES      SD ++L  LQ+ L+E +   +R+ LVLDDVW+E++ W  L A L+
Sbjct: 252  TKEIIESATKVEQSDKLNLDTLQQLKEKIASERFLLVLDDVWSENRRDDWERLCAPLRFA 311

Query: 281  ASGAFVLTTRLEKVGSIIMGTLPYELSNLSPEDCWFLFMQRAFGHQEEINP---NLVA 336
      A G+ V+ TTR  K+ SI+GT++   L  L  +   W LF + AFG      +NP      L
Sbjct: 312  ARGSKVIVTTRDTKIASIIGTMKEISLDGLQDDAYWELFKKCAFG---SVNPQEHLELEV 368

Query: 337  IGKEIVKKCGGVPLAAKTLGGILRFKREEREWEHV-DSPIWNLPQDESSILPALRLSYHH 395
      IG++I  K  G  PLAAKTLG +LR   + W  + +S +W LPQ E+ ILP L LSY H
Sbjct: 369  IGRKIAGKLGKGSPLAAKTLGSLRLDVSQEHWRTIMESEVWQLPQAENEILPVLWLSYQH 428

Query: 396  LPLDLQCFVYCAVFPKDTKMAKENLIAFWMAHGFLLSKGNLELEDV-----NEVWNELY 450
      LP  L QCF +CAVF KD      K  LI  W+A GF+  +GN  +EDV      +E+ N  +
Sbjct: 429  LPGHLRQCFAFCAVFHKDYLFYKHელიQTWIAEGFIAHQGNKRMEDVGSSYFHELVNRSF 488

Query: 451  LRVSSY----- 456
      + S +

```


Blast Result

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Sbjct: 489 FQESRWRGRYVMHDLIHDLAQFISVGECHRIDDDKSKETPSTTRHLSVALTEQMKLVDFS 548

Query: 457 -----SPSLLQKFXXXXXXXXXXXXXQLPSSIGDLV 488
SL ++ +LP IGD+

Sbjct: 549 GYNKLRTLMINNQRNQPYMTKVNSCLLPKSLFKRLKRIHVVLVQKCGMKELPDIIGDLI 608

Query: 489 HLRYLDLSGNFRIRNLPKRLCKLQNLQTLDLHYCDLSCLPKQTSKLGSLRNLLLDGCSL 548
LRYLD+S N I+ LP+ LC L NLQ L L C L P+ SKL +LR L ++ +

Sbjct: 609 QLRYLDISYNACIQRLPESLCDLYNLQALRLWGC-QLRSFPQGMKSLINLRQLRVED-EI 666

Query: 549 TSTPPRIGLLTCLKSLSCFVIGKRKGQYQLGELKNL-NLYGSISITKLDREVKKDSDAKEAN 607
S +G L L+ LS F + G +L EL L L ++ IT L+ V +A +A

Sbjct: 667 ISKIYEVGKLISLQELSAFKVLNNHGNKLAELSGLTQLRSTLRITNLENGVSKEEASKAK 726

Query: 608 LSAKANLHSLCLSW-----DLDGKHRYDSEVLEALKPHSNLKYLEINGFGGIRLPDWMN 661
L K L +L L W L+ + EVL L+PH LK L I G+ G +P W++

Sbjct: 727 LHRKQYLEALELEWAAGQVSSLEHELLVSEEVLLGLQPHHFLKSLTIRGYSGATVPSWLD 786

Query: 662 QSVLKNVVSIRIRGCENCSCLPFPGELPCLESLELHTGSADVEYVEDNVH-----PGR 714
+L N+ ++++ C L G+LP L+ L + + V+ H

Sbjct: 787 VKMLPNLGTCLKLENCTRLEGLSYIGQLPHLKVLHMKR----MPVVKQMSHELGCCTKSKL 842

Query: 715 FPSLRKLVIWDFSNLKGLLKKEGEEQFPVLEEMTFYWCPMFVIPTLSSVKTCLKVIATDAT 774
FP L +LV+ D LK +FP L + +P L + + A

Sbjct: 843 FPRLEELVLEDMPTLK-----EFPNLAQ-----LPCLKIHMKNMFAVKHI 883

Query: 775 VLRSISNLRALTSLDISNNVEATSLPEEMFKSLANLKYLNISFFRNKEL 824

++ + L + V L E +L L +L + +N+ L

Sbjct: 884 GRELYGDIESNCFSLSEELVLQDMLTLEELPNLGLPHLKVIHMKNMKSAL 933

Score = 38.9 bits (89), Expect = 1.2

Identities = 38/162 (23%), Positives = 66/162 (40%), Gaps = 16/162 (9%)

Query: 718 LRKLVIWDFSNLKGLLKKEGEEQFPVLEEMTFYWCPMFVI---PTLSSVKTCLKVIATDAT 774
L++L N GL EG + L+ + CP ++ V +L ++ D T

Sbjct: 1258 LKELGTVRIENCDGLGSIEGLQVLKSLKRLAIIGCPRLLLNEGDEQGEVLSLLELSVDKT 1317

Query: 775 VLRSISNLRALTSLDISNNVEATSLPE-----EMFKSLANLKYLNISFFRNKELP 825
L +S ++ +L +++ P+ E+ SL L+ L +NL+ LP

Sbjct: 1318 ALLKLSLIK--NTLPFIHSLRIIWSPQKVMFDLEEQLVHSLTALRRLEFFRCKNLQSLP 1375

Query: 826 TXXXXXXXXXXXXXFEFCNALESIPAEGVKGLTSLTELSVSNC 867

T C ++SLP +G+ T LT+L +C

Sbjct: 1376 TELHTLPSLHALVVSDCPQIQSLPEKGLP--TLLTDLGFDHC 1415

CPU time: 0.22 user secs. 0.00 sys. secs 0.22 total secs.

Lambda K H
0.320 0.137 0.410

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 9464

Number of extensions: 6271

Number of successful extensions: 20

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's gapped: 10

Number of HSP's successfully gapped: 2

Number of extra gapped extensions for HSPs above 10.0: 0

Blast Result

Length of query: 918
Length of database: 765,028,816
Length adjustment: 140
Effective length of query: 778
Effective length of database: 765,028,676
Effective search space: 595192309928
Effective search space used: 595192309928
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 81 (35.8 bits)



Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ Align

PRIOR ART

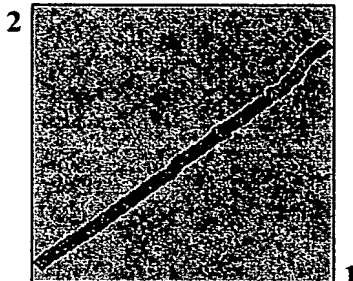
CLAIMED

Sequence 1 lcl|seq_1 Length 942 (1 .. 942)

D1 SEQ ID NO: 43

SEQ ID NO: 4

Sequence 2 lcl|seq_2 Length 1232 (1 .. 1232)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 403 bits (1035), Expect = e-110

Identities = 309/998 (30%), Positives = 486/998 (47%), Gaps = 126/998 (12%)

Query: 23 DDILDDCKTEAARFK--QAVLGRYHPRTITFCYKVGKRMKEMMEKLDIAIEERR-NPHLD 79
DDILD+ + A R K ++ R I + ++ ++ ++L+ + ER N
Sbjct: 82 DDILDEYEAAAIRLKVTRSTFKRLIDHVI-INVPLAHKVADIRKRLNGVTLERELNLGAL 140

Query: 80 ERIIERQAARRQ-TGFVLTEPKVYGREKEEDEIVKILINNVSYSEEVVPLPILGMGGLGK 138
E + +R T +LTE + GR ++++ ++L+ + VPV+PI+G+GG GK
Sbjct: 141 EGSQPLDSTKRGVTTSLTESCIVGRAQDKENLIRLLLEPSDGA--VPVPIVGLGGAGK 198

Query: 139 TTLAQMVFNDRITEHFNKIVWCVSDDFDEKRLIKAIVE-SIEGKSLGDMDLAPLQKKL 197
TTL+Q++FND+R+ EHF L++WVCVSDDFD KR+ + I E + G+ + +L LQ L
Sbjct: 199 TTLSQLIFNDRKVEEHFPLRMWVCVSDDFDVKRITREITEYATNGRFMDLTNLNMLQVNL 258

Query: 198 QELLNGKRYFLVLDDVWNEDQEKWDNLRAVLKIGASGASILITRLEKIGSIMGTLQLYQ 257
+E + G + LVLDDVWNED KW++L A L G G+ +++TT+ +K+ + GT++ Y
Sbjct: 259 KEEIRGTTFLVLDDVWNEDPVKWESLLAPLDAGGRGSVVIVTTQSKKVADVTGTMEPYV 318

Query: 258 LSNLSQEDCWLLFKQRAFCHQT--ETSPKLMEIGKEIVKKCGGVPLAAKTLGGLLRFKRE 315
L L+++D W L + +F + T+P++ EIG++I KK G+P A +G LR K
Sbjct: 319 LEELTEDDSWSLIESHSFREASCSSTNPRMEEIGRKIAKKISGLPYGATAMGRYLRSKHG 378

Query: 316 ESEWEHVRDSEIWNLPQDENSVLPA RLRSYHHLPLDLRQCFAYCAVFPKDTKIEKEYLIA 375
ES W V ++E W +P + VL ALR SY +LP L+ CFA+CA+F K + K+ LI
Sbjct: 379 ESSWREVLETETWEMPPAASDVLSALRRSYDNLPQLKLCFAFCALFTKGYRFRKDTLIH 438

Query: 376 LWMAHSFLLSKGNMELEDVGNEVWNELYLRSFFQEIEVKS GKTYFKMHDLIHDLX----- 430
+W+A + + S + ED+ E +++L R FF + + M+D +HDL
Sbjct: 439 MWIAQNLIQSTESKRSEDMAEECFDDLVCRRFF-----RYSWGNVYMNDSVHDLARWVSL 493

Query: 431 -----XXXXXXXXXXXXXIRQI----- -NVKDE-----DMMFIVTNYKDMMSIGFSEVV 473
IR + NV +D D + +++ + ++ +G SE
Sbjct: 494 DEYFRADEDSPLHISKPIRHLWCSEIRITNVLEDNNTGGDAVNPLSSLRTLLFLGQSEFR 553

Query: 474 SSY-SPSLFKRFVSLRVLNLSNSEFEQLPSSVGDLVHLRYLDLSGNKICSLPKRLCKLQN 532
S + +F+ +RVL+ SN LPSSVG+L HRLYL LS +I LP+ + +L

Blast Result

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Sbjct: 554 SYHLLDRMFRMLSRIRVLDFSNCVIRNLPSSVGNLKHRLYLGLSNTRIQLRPESVTRLCL 613

Query: 533 LQTLDLYNCSLSCLPKQTSKLCSLRNVLVDHCPLTSMPPRIGLLTCLKTLGYFVVGERK 592
LQTL L C+ L LP+ S+L LR L + + + ++G L L+ L + V ++K

Sbjct: 614 LQTLLEEGCE-LCRLPRSMSRLVKLRQLKANPDVIADI-AKVGRLELQELKAYNVDKKK 671

Query: 593 GYQLGELRNLN-LRGAISITHLERVKNDMEAKEANLSAKANLHSLSMSW-DRPNRYESE- 649
G+ + EL +N L G +SI +L+ V+ E+++A L K L L + W D E +

Sbjct: 672 GHGIAELSAMNQLHGDL SIRNLQNVKTRSRKARLDEKQKLKLLDLRWADGRGAGECDR 731

Query: 650 EVKVLEALKPHPNLKYLEIIDFCGFCLPDWMNHSV LKNVVSILISGCENCSCLPFPGELP 709
+ KVL+ L+PHPNL+ L I + G P WM L N+ +I + C + LP G+L

Sbjct: 732 DRKVLKGLRPHPNLRELSIKYYGGTSSPSWMTDQYLPNMETIRLRSCARLTCLGQLH 791

Query: 710 CLESLELQDGSVEVEYV-----EDSGF-----LTRRRFPSLRKLHIGGFCNLKGLQR 756
L L + DG +V + E SGF L RR PSL + +

Sbjct: 792 ILRHLHI-DGMSQVRQINLQFYGTGEVSGFPLLELLNIRRMPSLEEWS-----EP 840

Query: 757 MKGAEQFPVLEEMKISDCPMF-----VFPTLSSVKKLE-----IWGEADAGGXXXXX 803
+ FP L ++ I DCP + PTL ++ G D

Sbjct: 841 RRNCCYFPRHLKLLIEDCPRLRNLPSPPTLEELRISRTGLVDLPGFHNGDVTNNVSL 900

Query: 804 XXXXXXXXKIFS-----NHTVTSLLEEMFK-----NLENLI----- 834
++ S H + +L F +LE+LI

Sbjct: 901 SLHVSECRELRSLSEGLLQHNLVALKTAFTDCDSLEFLPAEGFRTAISLESIMTNCPL 960

Query: 835 ---YLSVSFLENLK-----ELPTSLASLNNLKCLDIRYCYAXXXXXXXXXXXXXX 879
+L S LE+LK L T +L +L LDI+ C

Sbjct: 961 PCSFLLPSSLEHLKLQPCLYPNNNEDSLSTCFENLTSLSFLDIKDCPNLSSFPPLCQL 1020

Query: 880 XXXXXXFVEHCNMLKCLPEGLQHLTTLTSLKIRGCPQL 917
+ +C L+ + G Q LT+L SL I+ CP+L

Sbjct: 1021 SALQHLSLVNCQRLQSI--GFQALTSLESITIQCNPRL 1056

CPU time: 0.09 user secs. 0.00 sys. secs 0.09 total secs.

Lambda	K	H
0.321	0.138	0.416

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 7971

Number of extensions: 5184

Number of successful extensions: 25

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's gapped: 2

Number of HSP's successfully gapped: 1

Number of extra gapped extensions for HSPs above 10.0: 0

Length of query: 942

Length of database: 765,028,816

Length adjustment: 140

Effective length of query: 802

Effective length of database: 765,028,676

Effective search space: 613552998152

Effective search space used: 613552998152

Neighboring words threshold: 9

Window for multiple hits: 0

X1: 16 (7.4 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.9 bits)

S2: 82. (86.2 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ Align

PRIOR ART

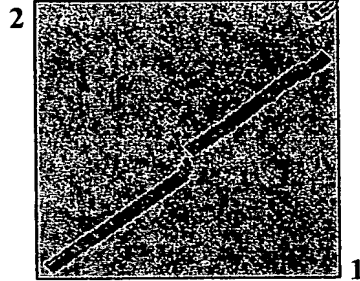
CLAIMED

Sequence 1 lcl|seq_1 Length 918 (1 .. 918)

D1 SEQ ID NO: 2

SEQ ID NO: 4

Sequence 2 lcl|seq_2 Length 1232 (1 .. 1232)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 389 bits (999), Expect = e-106

Identities = 303/949 (31%), Positives = 448/949 (46%), Gaps = 139/949 (14%)

Query: 42 AVLEDAQEKQLNDKPLENWLQKLNAATYEVDLILDEYKTKATRF--LQSEYGRYHPKVI- 98
++LE+A+ +++ DK L WL +L Y+ DDILDEY+ A R +S + R VI
Sbjct: 52 SLLEEAKARRMTDKSLVLWLMELKEWAYDADDILDEYEAAAIRLKVTRSTFKRLIDHVII 111

Query: 99 --PFRHKVKGKRMDDQVMKKLNIAIEERK-NFHLQEKIIERQAATRE-TGSVLTEPQVYGRD 154
P HKV + K+LN + ER+ N E + R T S+LTE + GR
Sbjct: 112 NVPLAHKVA---DIRKRLNGVTLERELNLGALEGSQPLDSTKRGVTTSLTESCIVGRA 167

Query: 155 KEKDEIVKILINNVSDAQKLSVLPIGLMGGLGKTTLSQMVFNDQRVTERFYPKIWICVSD 214
++K+ ++++L+ A + V+PI+G+GG GKTTLSQ++FND+RV E F ++W+CVSD
Sbjct: 168 QDKENLIRLLLEPSDGA--VPVPIVGLGGAGKTTLSQLIFNDKRVEEHFPLRMWVCVSD 225

Query: 215 DFDEKRLIKAIVE-SIEGKSLSDMDLAPLQKKLQELLNGKRYFLVLDDVWNEDQHKWANL 273
DFD KR+ + I E + G+ + +L LQ L+E + G + LVLDDVWNED KW +L
Sbjct: 226 DFDVKRITREITEYATNGRFMDLTNLNMLQVNLKEEIRGTTFLVLDDVWNEDPVKWESL 285

Query: 274 RAVLKVGASGAFVLTTTTRLEKVGSIIMGTLPYELSNLSPEDCWFLFMQRAFGHQ--EEIN 331
A L G G+ V+ TT+ +KV + GT++PY L L+ +D W L +F N
Sbjct: 286 LAPLDAGGRGSVVIVTTQSKKVADVTGTMEPYVLEELTEDDSWSLIESHSFREASCSSTN 345

Query: 332 PNLVAIGKEIVKKCGGVPLAAKTLGGILRFKREEREWEHV-DSPIWNLPQDESSILPALR 390
P + IG++I KK G+P A +G LR K E W V ++ W +P S +L ALR
Sbjct: 346 PRMEEIGRKIAKKISGLPYGATAMGRYLRSKHGESSWREVLETETWEMPPAASDVLSALR 405

Query: 391 LSYHHLPLDLQCFVYCAVFPKDTKMAKENLIAFWMAHGFLLSKGNLELEDV----- 442
SY +LP L CF +CA+F K + K+ LI W+A + S + ED+
Sbjct: 406 RSYDNLPPQLKLCFAFCALFTKGYRFRKDTLIHMWIAQNLIQSTESKRSEDMAEECFDDL 465

Query: 443 -----NEVWNEL-----YLRVSSYSPLLQK----- 463
N V N+ Y R SP + K
Sbjct: 466 VCRFFFRYSWGNVVMNDSVHDLARWVSLDEYFRADEDSPLHISKPIRHLWCSEIRITNVL 525

Query: 464 -----FXXXXXXXXXXXXXQLPSSI 484
LPSS+

Sbjct: 526 EDNNTGGDAVNPLSSLRTLLFLGQSEFRSYHLLDRMFRMLSRIRVLDIFSNCVIRNLPSSV 585

Query: 485 GDLVHLRYLDLSGNFRIRNLPKRLCKLQNLQTLDLHYCDLSCLPKQTSKLGSLRNLLLD 544
G+L HLRYL LS N RI+ LP+ + +L LQTL L C+ L LP+ S+L LR L +

Sbjct: 586 GNLKHLRYLGLS-NTRIQRLPESVTRLCLLQTLLEGECE-LCRLPRSMSRLVKLRQLKAN 643

Query: 545 GCSLTSTPPRIGLLTCLKSLSCFVIGKRKGQYQLGELKNLN-LYGSISITKLDREVKKDSDA 603
+ + +G L L+ L + + K+KG+ + EL +N L+G +SI L V+K ++

Sbjct: 644 P-DVIADIAKVGRILIELQELKAYNVDDKKKGHIAELSAMNQLHGDLISIRNLQNVEKTRES 702

Query: 604 KEANLSAKANLHSLCLSWDLGDKHR----YDSEVLEALKPHSNLKYLEINGFGGIRLPDW 659
++A L K L L L W DG+ D +VL+ L+PH NL+ L I +GG P W

Sbjct: 703 RKARLDEKQKLKLLDLRW-ADGRGAGECDRDRKVLKGLRPHPNLRELSIKYYGGTSSPSW 761

Query: 660 MNQSVLKNVVSIRIRGCENCSCLPFPGELPCLESLELHTGSADVEYVEDNVH----PGRF 715
M L N+ +IR+R C + LP G+L L L + G + V + + F

Sbjct: 762 MTDQYLPNMETIRLRSCARLTCLGQLHILRHLHI-DGMSQVRQINLQFYGTGEVSGF 820

Query: 716 PSLRKLVIWDFSNLKGLLK-KEGEEQFPVLEEMTFYWCP-MFVIPTLSSVTKLVIATDA 773
P L L I +L+ + + FP L ++ CP + +P+L TL+ +

Sbjct: 821 PLLELLNIRRMPSLEEWSEPRNCCYFPRHLKLLIEDCPRLRNLPSP--PTLEELRISR 878

Query: 774 TVLRSISNLRALTSLDISNNVEATSLPEEMFKSLANLKYLNISFFRNKELPTXXXXXXX 833
T L + + D++ NV +SL + L +L + NL L T

Sbjct: 879 TGLVDLPFGFHG--NGDVTTNVSLSLHVSECRELRSLSEGLLQ--HNLVALKT----- 927

Query: 834 XXXXXFEFCNALESIPAEGVKGLTSLTELSVSNMMLKC---LPEGLQH 879

F C++LE LPAEG + SL L ++NC L C LP L+H

Sbjct: 928 ---AAFTDCDSLEFLPAEGFRTAISLESIMTNC-PLPCSFLLPSSLEH 972

Score = 43.9 bits (102), Expect = 0.036

Identities = 24/75 (32%), Positives = 37/75 (49%), Gaps = 1/75 (1%)

Query: 842 CNALESIPAEGVKGLTSLTELSVSNMMLKCLPEGLQHXXXXXXXXXXQCPIVFKRCERGI 901
C LE LPA ++ L SL+ L + C + P G +CP + +RC+

Sbjct: 1148 CPNLEVL PAN-LQSLCSLSTLYIVRCPRIHAFPPGGVSM SLAHLVIHECPQLCQRCDPPG 1206

Query: 902 GEDWHKIAHIPYLT 916

G+DW IA++P + L

Sbjct: 1207 GDDWPLIANVPRICL 1221

CPU time: 0.15 user secs. 0.01 sys. secs 0.16 total secs.

Lambda K H
0.320 0.137 0.410

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 7820

Number of extensions: 5118

Number of successful extensions: 24

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's gapped: 7

Number of HSP's successfully gapped: 2

Number of extra gapped extensions for HSPs above 10.0: 0

Length of query: 918

Length of database: 765,028,816

Length adjustment: 140

Effective length of query: 778

Blast Result

Effective length of database: 765,028,676
Effective search space: 595192309928
Effective search space used: 595192309928
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits) **
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 81 (35.8 bits)



Blast 2 Sequences results

PubMed

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Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: 1 | Mismatch: -2 | gap open: 5 | gap extension: 2
x_dropoff: 50 | expect: 10.000 | wordsize: 11 | Filter ☒ | Align

Bior Art

Claimed

Sequence 1 lcl|seq_1 Length 6658

D2

SEQ ID NO: 1

Sequence 2 lcl|seq_2 Length 4380

No significant similarity was found

**Blast 2 Sequences results**

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x_dropoff: 50 expect: 10.0001 wordsize: 11 ☐ Filter ☐ Align

Sequence 1 lcl|seq_1 Length 6658

Sequence 2 lcl|seq_2 Length 3660

No significant similarity was found

Prior Art
*D2**Claimed*
SEQ ID NO: 3



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ Align

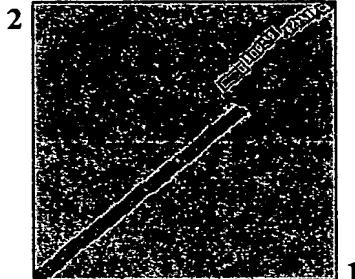
Prior Art

Claimed
SEQ ID NO: 2

Sequence 1 lcl|seq_1 Length 1266 (1 .. 1266)

D2

Sequence 2 lcl|seq_2 Length 1441 (1 .. 1441)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 478 bits (1231), Expect = e-133

Identities = 319/896 (35%), Positives = 479/896 (52%), Gaps = 47/896 (5%)

```
Query: 1  MEIGLAVGGAFLLSSALNVLFDR LAPNGDLLNMFRXXXXXXXXXXXXMTLRGIQIVLSDA 60
      M  L +GG F S + L D+ A N + + R LR I +L A
Sbjct: 1  MSTALVIGGWFAQSF IQTLLDK-ASNC AIQQ LARRRGLHDDLRLRLRTSLLR-IHAILDKA 58

Query: 61  ENK-QASNPSVRDWLNELRDAVDSAENLIEEVN YEALRLKVEGQHQNFS ETSNQQVS--- 116
      E + N S+ + + +L+DA AE+L+EE+ Y+A + KVE + S+ + +S
Sbjct: 59  ETRWNHKNTSLVELVRQLKDAAYDAEDLLEELEYQA AKQKVEHRGDQISDLFSFSLSTAS 118

Query: 117  -----DDFFLN IKDKLED TIETLKD LQEQIGLLGLKE---YFDSTKLETRRPSTSVDD 166
      DD +++ D+ + + LL + FD + RR ++S
Sbjct: 119  EWL GADGDDAGTRLREIQGKLCNIAADMM DVMQLLAPDDGGRQFDWKV--RRETSSFLT 176

Query: 167  ESDIFGRQSEIEDLIDRLLSEGASGKKLT VVPIVGMGGQKTTLAKAVYNDERVKNHFDL 226
      E+ +FGR E E +++ LL G+ +V+P+VG+GG GKTTLA+ VYND RV N+F L
Sbjct: 177  ET VVFGRDQEREKVV ELLLD SSGSNSSFSV LPLVGIGGVGKTTLAQLVYNDNRVGN YFHL 236

Query: 227  KAWYCVSEGF DALRITKELLQEIGKFD SKDVHNNLNQLQVKLKESLKGKKFLIVLDDVWN 286
      K W CVS+ F+ R+TKE+++ K + D NL+ LQ LKE + ++FL+VLDDVW+
Sbjct: 237  KVVVCVSDNFNVKRLTK EII ESATKVEQSD- KLNLDTLQQILKEKIASERFLLVLDDVWS 295

Query: 287  ENYNEWNDLRNIFAQGDIGSKIIVTTRKDS VALMMGN-EQIRMGNLSTEASWSLFQRHAF 345
      EN ++W L GSK+IVTTR +A ++G ++I + L +A W LF++ AF
Sbjct: 296  ENRDDWERLCAPLRFAARGSKVIVTTRDTKIASIIGTMKEISLDGLQDDAYWELFKKCAF 355

Query: 346  ENMDPMGHP EEEVGRQIAAKCKGLPLALK TLAGMLRSKSEVEEWKRILRSEIWELP--H 403
      +++P H ELE +GR+IA K KG PLA KTL +LR E W+ I+ SE+W+LP
Sbjct: 356  GSVNPQEHLELEVIGRKIAGK LKGSPLAAKT LGSLLRLDVSQEHWR TIMESEVWQLPQAE 415

Query: 404  NDILPALMLS YNDLPAHLKRCFSFCAIFPKDY PFRKEQVIHLWIANGLV PVK-DEINQDL 462
      N+ILP L LSY LP HL++CF+FCA+F KDY F K ++I WIA G + + ++ +D+
Sbjct: 416  NEILPVLWLSYQHLPGHLRQCFAFC AVFHKDYLFYKHELIQTWIAEGFIAHQGNKR MEDV 475

Query: 463  GNQYFLELRSRSLFEKVPNP SKRNIEELFLMHDL VNDLAQLASSKLCIRLEESQGS HMLE 522
      G+ YF EL +RS F+ + ++MHD L++DLAQ S C R+++ +
```


Sbjct: 476 GSSYFHELVNRSFFQ-----ESRWRGRYVMHDLIHDLAQFISVGECHRIDDDKSKETPS 529

Query: 523 QCRHLSYSIGFNGEFKKLTPLYKLEQLRTLLPIRIEFRLHNLKSK---RVLHNLPLTLRS 578
RHLS ++ E KL +LRTL+ + ++K + H++ L+

Sbjct: 530 TTRHLSVAL---TEQMKLVDFSGYNKLRTLMINNQRNQPYMTKVNLSCLLPHSLFKRLKR 586

Query: 579 LRALSFSQYKIKELPNDLFTKLKLLRFLDIS-RTWITKLPDSICGLYNLETLLLSSCADL 637
+ L + +KELP D+ L LR+LDIS I +LP+S+C LYNL+ L L C L

Sbjct: 587 IHVLVLQKCGMKELP-DIIGDLIQLRYLDISYNACIQLRPESLCDLYNLQALRLWGC-QL 644

Query: 638 EELPLQMEKLINLRHLDVSNTRRLKMPLHLSRLKSLQVLVGPKEFFVD-GWRMEDLGEAQN 696
P M KLINLR L V + K+ + +L SLQ L K + G ++ +L

Sbjct: 645 RSFPQGMKSLINLRQLRVEDEIISKI-YEVGKLISLQELSAFKVLNNHGNKLAELSGLTQ 703

Query: 697 LHGSLSVVKLENVVDREAVKAKMREKNHVEQLSLEWSE---SSIADNSQTESDILDEL 753
L +L + LENV + EA KAK+ K ++E L LEW+ SS+ ++L L

Sbjct: 704 LRSTLRITNLENVGSKEEASKAKLHRKQYLEALELEWAAGQVSSLEHELLVSEEVLGLQ 763

Query: 754 PHKNIKKVEISGYRGTFNPNWVADPLFLKLVNLSLRNCKDCYSLPALGQLPCLKFLSVKG 813
PH +K + I GY G P+W+ + L L L NC L +GQLP LK L +K

Sbjct: 764 PHHFLKSLTIRGYSGATVPSWLDVKMLPNLGLTKLENCTRLEGLSYIGQLPHLKVLMKR 823

Query: 814 MHGIRVVTEEFYGRLSKKPFNSLEKLEFEDMTEWKQWHALGIGEFPTLENLSIKN 869
M ++ ++ E G SK F LE+L EDM K++ + + P L+ + +KN

Sbjct: 824 MPVVKQMSHELGCCTKSKL-FPRLEELVLEDMPVLKEFP--NLAQLPCLKIIHMKN 876

Score = 79.3 bits (194), Expect = 1e-12
Identities = 124/517 (23%), Positives = 191/517 (35%), Gaps = 142/517 (27%)

Query: 780 FLKLVNLSLRNCKDCYSLPALGQLPCLKFLSVKGMHGIRVVTEEFYGRLSKKPFNSLEK 839
F +L L ++ L +L +LPCLK +KG+ ++ + + ++ F LE

Sbjct: 997 FPRLEELEIKGMLTFEELHSLEKLPCLKVFRIGLPAVKKIGHGLFDSTCQRECFPRLED 1056

Query: 840 LEFEDMTEWKQWHALGIGE-FPTLENLSIKNCPELSLEIPIQFS----- 882
L DM W++W E F L L I+ CP+L +PI S

Sbjct: 1057 LVLSDMPAWEESWAEREELFSLCRLKIEQCPKLKCLLPPIPHSLIKLELWQVGLTGLPG 1116

Query: 883 -----SLKRLEVSDCPVVFDDAQLFRSQLEAMKQIEEIDICDCNSVTSFPP 928
SL L + CP + + + S + I I I +C + P

Sbjct: 1117 LCKGIGGSSTRTASLSLHIIKCPNLRNLGEGLLS--NHLPHINAIRIWECAELLWLPV 1174

Query: 929 SILP--TTLKRIQISRCPKLKLEAPVGE-----MFVEYLRVNDGCGVDDISP---EFLP 977
TTL+ + I CPKL E ++ L + DCG + P L

Sbjct: 1175 KRFREFTTLENLSIRNCPKLMSMTQCEENDLLLPPLIKALELGDGNGKSLPGCLHNLS 1234

Query: 978 TARQLSIENCQ--NVTRFLIPTATE--TLRISNCENVEKLSVACGGAAQMTSLNIWGX 1032
+ QL+I NC ++ R ++ E T+RI NC+ +

Sbjct: 1235 SLTQLAISNCPYMVSLPREVMLHLKELGTVRIENC DGL----- 1272

Query: 1033 XXXXXXXXXXXXXXXXXXXDCPEIEG-ELPFNLEILRIIYCKKLKLV--NGRKEWHLQRLTEL 1089
IEG ++ +L+ L II C +L+ G ++ + L EL

Sbjct: 1273 -----GSIEGLQVLKSLKRLAIIGCPRLLLNEGDEQGEVLSLLEL 1312

Query: 1090 WIDHDGSDIEDIEHWELPCSIQRLTIKNLKTLSQHLKSLTSLOQLCIEGYLXXXXXXXX 1148
+D ++ IKN TL H L+ + S Q + +

Sbjct: 1313 SVDK-----TALLKLSLIK--TLPFIHSLRIIWSPQKVMFD-----LEE 1350

Query: 1149 XXXXXHLTSLQTLQIWNFLNXXXXXXXXXXXXXXXXXIDDCPNLQSL-FESALPSSLSQL 1207
LT+L+ L+ + C NLQSL E SL L

Sbjct: 1351 QELVHSLTALRRLEFFR-----CKNLQSLPTELHTLPSLHAL 1387

Query: 1208 FIQDCPNLQSLPFGMPSSLSKLSIFNC-PLLTPLLE 1243
+ DCP +QSLP KG+P+ L+ L +C P+LT LE

Sbjct: 1388 VVSDCPQIQSLPEKGLPTLLTDLGFDHCHPVLTAQLE 1424

CPU time: 0.21 user secs. 0.00 sys. secs 0.21 total secs.

Blast Result

Lambda	K	H
0.320	0.137	0.408

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 13,460

Number of extensions: 8847

Number of successful extensions: 46

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's gapped: 5

Number of HSP's successfully gapped: 2

Number of extra gapped extensions for HSPs above 10.0: 0

Length of query: 1266

Length of database: 765,046,178

Length adjustment: 142

Effective length of query: 1124

Effective length of database: 765,046,036

Effective search space: 859911744464

Effective search space used: 859911744464

Neighboring words threshold: 9

Window for multiple hits: 0

X1: 16 (7.4 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.8 bits)

S2: 83 (36.6 bits)



Blast 2 Sequences results

PubMed

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BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ Align ☐

Prior Art

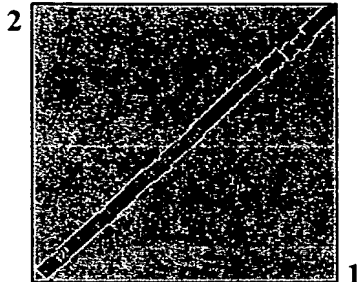
Claimed

D2

SEQ ID NO: 4

Sequence 1 lcl|seq_1 Length 1266 (1 .. 1266)

Sequence 2 lcl|seq_2 Length 1232 (1 .. 1232)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 469 bits (1206), Expect = e-130

Identities = 389/1271 (30%), Positives = 597/1271 (46%), Gaps = 157/1271 (12%)

Query: 49 TLRGIQIVLSDAENKQASNPVSRDNLNELRDAVDSAENLIEEVNVEALRLKVEGQHQNFS 108
TL +L +A+ ++ ++ S+ WL EL++ A+++++E A+RLKV +
Sbjct: 46 TLLRTHSLLEEAKARRMTDKSLVLWLMELKEWAYDADDILDEYEAAAIRLKV-----T 98

Query: 109 ETSNQVQSDDFFLNIK--DKLEDTIETLKDL---QEIGLLGLKEYFDSTKLETRRPST 162
++ +++ D +N+ K+ D + L + + +G L + DSTK R +T
Sbjct: 99 RSTFKRLIDHVIINVPLAHKVADIRKRLNGVTLERELNLGALEGSQPLDSTK---RGVTT 155

Query: 163 SVDDSDIFGRQSEIEDLIDRLSEGASGKKLTVPVIVGMGGQKTTLAKAVYNDERVKN 222
S+ ES I GR + E+LI RLL E + G + VVPIVG+GG GKTTL++ ++ND+RV+
Sbjct: 156 SLLTESCIVGRAQDKENLI-RLLLEPSDGA-VPVPIVGLGAGKTTLSQLIFNDKRVEE 213

Query: 223 HFDLKAWYCVSEGFDA LRITKELLQEIGKFDSKDVHNNLNQLQVKLKESLKGKKFLIVLD 282
HF L+ W CVS+ FD RIT+E+ + D+ NLN LQV LKE ++G FL+VLD
Sbjct: 214 HFPLRMWVCVSDDFDVKRITREITEYATNGRFMDL-TNLNMLQVNLKEEIRGTTFLVLVD 272

Query: 283 DVWNNYNEWNLRLNIFAQGDIGSKIIVTTRKDSVALMMGN-EQIRMGNLSTEASWSLFQ 341
DVWNE+ +W L G GS +IVTT+ VA + G E + L+ + SWSL +
Sbjct: 273 DVWNEDPVKWESLLAPLDAGGRGSVVIVTTQSKKVADVTGTMEPYVLEELTEDDSWSLIE 332

Query: 342 RHAFENMDPMG-HPELEEVGRQIAACKGLPLALKTLAGMLRSKSEVEEWKRILRSEIWE 400
H+F +P +EE+GR+IA K GLP + LRSK W+ +L +E WE
Sbjct: 333 SHSFREASCSSTNPRMEEIGRKIAKKISGLPYGATAMGRYLRSKHGESSWREVLETETWE 392

Query: 401 LPH--NDILPALMLSYNLPAHLKRCFSFCAIFPKDYPFRKEQVIHLWIANGLV-VKDE 457
+P +D+L AL SY++LP LK CF+FCA+F K Y FRK+ +IH+WIA L+ + +
Sbjct: 393 MPAAASDVLSALRRSYDNLPPQLKLCFAFCALFTKGYRFRKDTLIHMIWIAQNLIQSTESK 452

Query: 458 INQDLGNQYFLELRSLFEKVPNPSPKRNIEELFLMHDLVNDLAQLASSKLCIRLEESQG 517
++D+ + F +L R F R ++M+D V+DLA+ S R +E
Sbjct: 453 RSEDMAEECFDDLVCRRFF-----RYSWGNVNMNSVHDLARWVSLDEYFRADEDS 504

Query: 518 SHMLEQCRHLSYSIGFNGEFKLTPLYK-----LEQLRTLLPI-RIEFRLHNLS 565
H+ + RHLS+ +++T + + L LRTLL + + EFR ++L

Blast Result

Sbjct: 505 LHISKPIRHLWC-----ERITNVLEDNNTGGDAVNPLSSLRTLLFLGQSEFRSYHLL 558

Query: 566 KRVLHNILPTLRSLRALSFSQYKIKELPNDLFTKLKLLRFLDISRTWITKLPDSICGLYN 625
R+ L +R L FS I+ LP+ + LK LR+L +S T I +LP+S+ L

Sbjct: 559 DRMFR---MLSRIRVLDIFSNCVIRNLPSSV-GNLKHLRYLGLSNTRIQLRPESVTRLCL 613

Query: 626 LETLLSSCADLEELPLQMEKLINLRHLDVSNTRRLKMPHLHSLKSLQVLVGPKEFFVD- 684
L+TLL C +L LP M +L+ LR L +N + + RL LQ L + VD

Sbjct: 614 LQTLLEGC-ELCRLPRMSRLVKLRQLK-ANPDVIADIAKVGRLLIELQELKA--YNVDK 669

Query: 685 --GWRMEDLGEAQNHLHGSLSVVKLENVVDREAVKAKMREKNHVEQLSLEWSESSIADNS 742
G + +L LHG LS+ L+NV RE+ KA++ EK ++ L L W++ A

Sbjct: 670 KKGHGIAELSAMNQLHGDLIRNLQNVEKTRESRKARLDEKQKLKLLDLRWADGRGAGEC 729

Query: 743 QTESDILDELCPHKNIKKVEISGYRGTFNPNWVADPLFLKLVNLSLRNCKDCYSLPALGQ 802
+ +L L PH N++++ I Y GT+ P+W+ D + + LR+C LP LGQ

Sbjct: 730 DRDRKVLKGLRPHPNLRELSIKYYGGTSSPSWMTDQYLPNMETIRLRSCARLTLPCLGQ 789

Query: 803 LPCLKFLSVKGMHGIRVVTEEFYGRSSKKPFNSLEKLEFEDMTEWKQWH--ALGIGFP 860
L L+ L + GM +R + +FYG F LE L M ++W FP

Sbjct: 790 LHILRHLHIDGMSQVRQINLQFYG-TGEVSGFPLLELLNIRRMPSLEEWSEPRRNCYFP 848

Query: 861 TLENLSIKNCPELSLEIPIQFSSLRLEVS DCPVVFDDAQLFRSQLEAMKQIEEIDICDC 920
L L I++CP L +P +L+ L +S +V + + + +C

Sbjct: 849 RLHKLLIEDCPRLR-NLPSLPPTLEELRISRTGLVDLPGFHNGDVTNNVSLSLHVSEC 907

Query: 921 NSVTSFPFSILPTTLKRIQISRCPKLKLEAPVGEMFVEYLRVNDCGCVDDISPEFLPTA- 979
+ S +L L ++ + DC ++ + E TA

Sbjct: 908 RELRSLSEGLLQHNLVALKTA-----AFTDCDSLEFLPAEGFRTAI 948

Query: 980 --RQLSIENCQNVTRFLIPTATETLRISNC---ENVEKLSVACGGAAQMTSLNIWGX XX 1033
L + NC FL+P++ E L++ C N + LS ++ L+I

Sbjct: 949 SLESLIMTNCPLPCSFLPSSLEHLKLQPCLYPNNEDSLSTCFENLTSLSFLDI----- 1003

Query: 1034 XXXXXXXXXXXXXXXXXXXDCPEIEGELPFNLEILRIIYCKKLVNGRKEWHLQRLTELWIDH 1093
DCP + P L L + LVN QRL +

Sbjct: 1004 -----KDCPNLSSFPPLCQLSALQHLSLVN-----CQRLQSI----- 1037

Query: 1094 DGSDEIDIEHWELPCSIQRLTIKNLKTLSQHL-----KSLTSLQYLCI-----EG 1138
++ S++ LTI+N L+ H S T L + +G

Sbjct: 1038 -----GFQALTSLES LTIQNCPRLTMSHSLVEVNSSDTGLAFNITRWMRRRTGDDG 1089

Query: 1139 YL---XXXXXXXXXXXXHLTSLQTLQIWN-----FLNXXXXXXXXXXXXXXXXXIDDCP 1190
+ HLT LQ L+I I DCP

Sbjct: 1090 LMLRHRAQNDSFFGGLLQHLTFLQLKICQCPQLVTFTGEEEEKWRNLTSLQILHIVDCP 1149

Query: 1191 NLQSLFESALPS--SLSQLFIQDCPNLQSLPFGMPSSLSKLSIFNCPLLTPLLEFDKGE 1248
NL+ L + L S SLS L+I CP + + P G+ SL+ L I CP L + G+

Sbjct: 1150 NLEVL-PANLQSLCSLSTLYIVRCPRIHAFFPPGGVMSLAHLVIHECPQLCQRCDPPGGD 1208

Query: 1249 YWPQIAHIPII 1259
WP IA++P I

Sbjct: 1209 DWPLIANVPRI 1219

CPU time: 0.09 user secs. 0.01 sys. secs 0.10 total secs.

Lambda K H
0.320 0.137 0.408

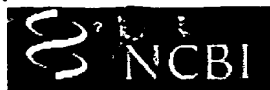
Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 10,906

Blast Result

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Number of extensions: 7195
Number of successful extensions: 35
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 1266
Length of database: 765,046,178
Length adjustment: 142
Effective length of query: 1124
Effective length of database: 765,046,036
Effective search space: 859911744464
Effective search space used: 859911744464
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ Align

Prior Art

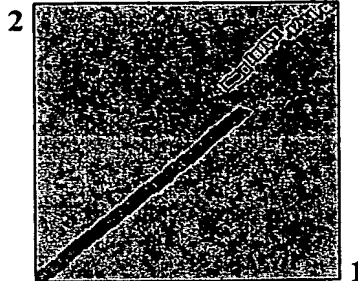
Claimed

Sequence 1 lcl|seq_1 Length 1266 (1 .. 1266)

D3

SEQ ID NO 2

Sequence 2 lcl|seq_2 Length 1441 (1 .. 1441)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 478 bits (1231), Expect = e-133

Identities = 319/896 (35%), Positives = 479/896 (52%), Gaps = 47/896 (5%)

```
Query: 1  MEIGLAVGGAFLLSSALNVLFDR LAPNGDLLNMFRXXXXXXXXXXXXMTLRGIQIVLSDA 60
      M  L +GG F S + L D+ A N + + R LR I +L A
Sbjct: 1  MSTALVIGGWFAQSF IQTLLDK-ASNCAIQQLARRRGLHDDLRLRLRTSLLR-IHAILDKA 58

Query: 61  ENK-QASNPSVRDWNELRDAVDSAENLIEEVNYEALRLKVEGQHQNFS ETSNQQVS--- 116
      E + N S+ + + +L+DA AE+L+EE+ Y+A + KVE + S+ + +S
Sbjct: 59  ETRWNHKNTSLVELVRQLKDAAYDAEDLLEELEYQA AKQKVEHRGDQISDLFSFSLSTAS 118

Query: 117  -----DDFFLNKDKLEDTIETLKD LQEIGLLGLKE---YFDSTKLETRRPSTSVDD 166
      DD +++ D+ + + LL + FD + RR ++S
Sbjct: 119  EWL GADGDDAGTRLREIQGKLCNIAADMMDVMQL LAPDDGGRQFDWKVV--RRETSSFLT 176

Query: 167  ESDIFGRQSEIEDLIDRL LSEGASGKKLT VVPIVGMGGQGKTT LAKAVYNDERVKNHFDL 226
      E+ +FGR E E +++ LL G+ +V+P+VG+GG GKTTLA+ VYND RV N+F L
Sbjct: 177  ETVVFG RDQEREKVV ELLLD SSGNSSFSVLPV LGIGGVGKTTLAQLVYNDNRVGN YFHL 236

Query: 227  KAWYCVSEGF DALRITKELLQEIGKFDSKDVHNNLNQLQVKLKESLKGKKFLIVLDDVWN 286
      K W CVS+ F+ R+TKE+++ K + D NL+ LQ LKE + ++FL+VLDDVW+
Sbjct: 237  KVVVCVSDNFNVKRLTKEIIESATKVEQSD-KLNLDTLQQILKEKIASERFLLVLDDVWS 295

Query: 287  ENYNEWNDLRNIFAQGDIGSKIIVTTRKDSVALMMGN-EQIRMGNLSTEASWSLFQRHAF 345
      EN ++W L GSK+IVTTR +A ++G ++I + L +A W LF++ AF
Sbjct: 296  ENRDDWERLCAPLRFAARGSKVIVTTRDTKIASIIGTMKEISLDGLQDDAYWELFKKCAF 355

Query: 346  ENMDPMGHPELEEVRQIAACKG LPLALKTLAGMLRSKSEVEEWKRILRSEIWELP--H 403
      +++P H ELE +GR+IA K KG PLA KTL +LR E W+ I+ SE+W+LP
Sbjct: 356  GSVNPQEHLELEVIGRKIAGK LKGSPLAAKTLGSLRLDVSQEHWR TIMESEVWQLPQAE 415

Query: 404  NDILPALMLS YNDLPAHLKRCFSFCAIFPKDY PFRKEQVIHLWIANGLVPVK-DEINQDL 462
      N+ILP L LSY LP HL++CF+FCA+F KDY F K ++I WIA G + + ++ +D+
Sbjct: 416  NEILPVLWLSYQHLPGHLRQCFAFCAV FHKDYLFYKHELIQTWIAEGFIAHQGNKR MEDV 475

Query: 463  GNQYFLELRSRSLFEKVPNP SKRNIEELFLMHD LVNDLAQLASSKLCIRLEESQGSHMLE 522
      G+ YF EL +RS F+ + ++MHD L++DLAQ S C R+++ +
```


Sbjct: 476 GSSYFHELVNRSFFQ-----ESRWRGRYVMHDLIHDLAQFISVGECHRIDDDKSKETPS 529

Query: 523 QCRHLSYSIGFNGEFKKLTPLYKLEQLRTLPIRIEFRLHNLK---RVLHNLPTLRS 578
RHLS ++ E KL +LRTL+ + ++K + H++ L+

Sbjct: 530 TTRHLSVAL---TEQMKLVDFSGYNKLRTLMINNQRNQYPYMTKVNSCLLPHSLFKRLKR 586

Query: 579 LRALSFSQYKIKELPNDLFTKLKLLRFLDIS-RTWITKLPDSICGLYNLETLLSSCADL 637
+ L + +KELP D+ L LR+LDIS I +LP+S+C LYNL+ L L C L

Sbjct: 587 IHVLVLQKCGMKELP-DIIGDLIQLRYLDISYNACIQRLPESLCDLYNLQALRLWGC-QL 644

Query: 638 EELPLQMEKLINLRHLDVSNTRRLKMPHLHLSRLKSLQVLVGPKFFVD-GWRMEDLGEAQN 696
P M KLINLR L V + K+ + +L SLQ L K + G ++ +L

Sbjct: 645 RSFPQGM SKLINLRQLRVEDEIISKI-YEVGKLISLQELSAFKVLNNHGNKLAELSGLTQ 703

Query: 697 LHGSLSVVKLENVVDRREAVKAKMREKNHVEQSLSEWSE---SSIADNSQTESDILDEL 753
L +L + LENV + EA KAK+ K ++E L LEW+ SS+ ++L L

Sbjct: 704 LRSTLRITNLENVGSKBEASKAKLHRKQYLEALELEWAAGQVSSLEHELLVSEEVLLGLQ 763

Query: 754 PHKNIKKVEISGYRGTFNPNWVADPLFLKLVNLSLRNCKDCYSLPALGQLPCLKFLSVKG 813
PH +K + I GY G P+W+ + L L L NC L +GQLP LK L +K

Sbjct: 764 PHHFLKSLTIRGYSGATVPSWLDVKMLPNLGTCLKLENCTRLEGLSYIGQLPHLKVLMHMR 823

Query: 814 MHGIRVVTEEFYGRLLSSKKPFNSLEKLEFEDMTEWKQWHALGIGEFPTLENLSIKN 869
M ++ ++ E G SK F LE+L EDM K++ + + P L+ + +KN

Sbjct: 824 MPVVKQMSHELGCCTKSKL-FPRLEELVLEDMP TLKEFP--NLAQLPCLKIIHMKN 876

Score = 79.3 bits (194), Expect = 1e-12

Identities = 124/517 (23%), Positives = 191/517 (35%), Gaps = 142/517 (27%)

Query: 780 FLKLVNLSLRNCKDCYSLPALGQLPCLKFLSVKGMHGIRVVTEEFYGRLLSSKKPFNSLEK 839
F +L L ++ L +L +LPCLK +KG+ ++ + + ++ F LE

Sbjct: 997 FPRLEELEIKGMLTFEELHSLEKLPCLKVFRIGLPAVKKIGHGLFDSTCQRECFPRLED 1056

Query: 840 LEFEDMTEWKQWHALGIGE-FPTLENLSIKNCPELSLEIPIQFS----- 882
L DM W++W E F L L I+ CP+L +PI S

Sbjct: 1057 LVLSDMPAWEESWAEREELFSCLCRLKIEQC PKLKCLLP IPHSLIKLELWQVGLTGLPG 1116

Query: 883 -----SLKRLEVS DCPVVFDDAQLFRSQLEAMQIEEIDICDCNSVTSFPF 928
SL L + CP + + + S + I I I +C + P

Sbjct: 1117 LCKGIGGGSSTRTASLSLHIIKCPNLRNLGEGLLS--NHLPHINAIRIWECAELLWLPV 1174

Query: 929 SILP--TTLKRIQISRC PKLKLEAPVGE-----MFVEYLRVND CGCVDDISP---EFLP 977
TTL+ + I CPKL E ++ L + DCG + P L

Sbjct: 1175 KRFREFTTLENLSIRNCPKLMSMTQCEENDLLLP LIKALELGDCGNLGKSLPGCLHNLS 1234

Query: 978 TARQLSIENCQ---NVTRFLIPTATE--TLRISNCENVEKLSVACGGAAQMTSLNIWGXX 1032
+ QL+I NC ++ R ++ E T+RI NC+ +

Sbjct: 1235 SLTQLAISNCPYMSVSLPREVMLHLKELGT VRIENC DGL----- 1272

Query: 1033 XXXXXXXXXXXXXXXXXXXDCPEIEG-ELPFNLEILRIIYCKKL V--NGRKEWHLQRLTEL 1089
IEG ++ +L+ L II C +L+ G ++ + L EL

Sbjct: 1273 -----GSIEGLQVLKSLKRLAIIGCPRLLLNEGDEQGEVLSLLEL 1312

Query: 1090 WIDHDGSDIEDIEHWELPCSIQRLTIKNLKTLS SQH-LKSLTSLQYLCIEGYLXXXXXXXXX 1148
+D ++ IKN TL H L+ + S Q + +

Sbjct: 1313 SVDK-----TALLKLSLIK N--TLPFIHSLRIIWS PQKVMFD-----LEE 1350

Query: 1149 XXXXXHLTSLQTLQIWNFLNXXXXXXXXXXXXXXXXXIDDCPNLQSL-FESALPSSLSQL 1207
LT+L+ L+ + C NLQSL E SL L

Sbjct: 1351 QELVHSLTALRRLEFFR-----CKNLQSLPTELHTLPSLHAL 1387

Query: 1208 FIQDCPNLQSLPFGMPSSLSKLSIFNC-PLLTPLLE 1243
+ DCP +QSLP KG+P+ L+ L +C P+LT LE

Sbjct: 1388 VVSDCPQIQSLPEKGLPTLLTDLGFDHCHPVLT AQLE 1424

CPU time: 0.20 user secs. 0.01 sys. secs 0.21 total secs.

Lambda	K	H
0.320	0.137	0.408

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 13,460

Number of extensions: 8847

Number of successful extensions: 46

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's gapped: 5

Number of HSP's successfully gapped: 2

Number of extra gapped extensions for HSPs above 10.0: 0

Length of query: 1266

Length of database: 765,046,178

Length adjustment: 142

Effective length of query: 1124

Effective length of database: 765,046,036

Effective search space: 859911744464

Effective search space used: 859911744464

Neighboring words threshold: 9

Window for multiple hits: 0

X1: 16 (7.4 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.8 bits)

S2: 83 (36.6 bits)



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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.0001 wordsize: 3 Filter ☒ Align

Prior Art

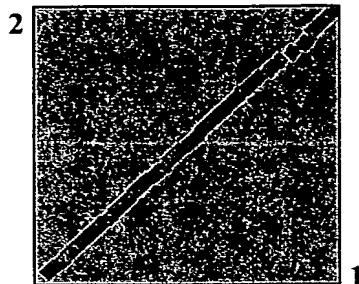
Claimed

Sequence 1 lcl|seq_1 Length 1266 (1 .. 1266)

D3

SEQ ID NO: 4

Sequence 2 lcl|seq_2 Length 1232 (1 .. 1232)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 469 bits (1206), Expect = e-130

Identities = 389/1271 (30%), Positives = 597/1271 (46%), Gaps = 157/1271 (12%)

Query: 49 TLRGIQIVLSDAENKQASNPVSRDWLNELRDAVDSAENLIEEVNYEALRLKVEGQHQNFS 108
 TL +L +A+ ++ ++ S+ WL EL++ A++++E A+RLKV +
 Sbjct: 46 TLLRTHSLLEEAKARRMTDKSLVLWLMELKEWAYDADDILDEYEAARLKV-----T 98

Query: 109 ETSNQVSDDFFLNIK--DKLEDTIETLKDL---QEIQIGLLGLKEYFDSTKLETRRPST 162
 ++ +++ D +N+ K+ D + L + + +G L + DSTK R +T
 Sbjct: 99 RSTFKRLIDHVIINVPLAHKVADIRKRLNGVTLERELNLEGALEGSQPLDSTK---RGVTT 155

Query: 163 SVDDSDIFGRQSEIEDLIDRLLSEGASGKKLTVPVIVGMGGQKTTAKAVYNDERVKN 222
 S+ ES I GR + E+LI RLL E + G + VVPIVG+GG GKTTL++ ++ND+RV+
 Sbjct: 156 SLLTESCIVGRAQDKENLI-RLLLEPSDGA-VPVPIVGLGGAGKTTLSQLIFNDKRVVEE 213

Query: 223 HFDLKAWYCVSEGFDA LRITKELLQEIGKFDSKDVHNNLNQLQVKLKESLKGKKFLIVLD 282
 HF L+ W CVS+ FD RIT+E+ + D+ NLN LQV LKE ++G FL+VLD
 Sbjct: 214 HFPLRMWVCVSDDFDVKRITREITEYATNGRFMDL-TNLNMLQVNLKEEIRGTTFLVLVD 272

Query: 283 DVWNNYNEWNLRLNIFAQGDIGSKIIVTTRKDSVALMMGN-EQIRMGNLSTEASWSLFQ 341
 DVWNE+ +W L G GS +IVTT+ VA + G E + L+ + SWSL +
 Sbjct: 273 DVWNEDPVKWESLLAPLDAGGRGSVVIVTTQSKKVADVTGTMEPYVLEELTEDDSWSLIE 332

Query: 342 RHAFENMDPMG-HPELEEVGRQIAACKGKLPLAKTLAGMLRSKSEVEEWKRILRSEIWE 400
 H+F +P +EE+GR+IA K GLP + LRSK W+ +L +E WE
 Sbjct: 333 SHSFREASCSTNPRMEEIGRKIAKKISGLPYGATAMGRYLRSKHGESSWREVLETETWE 392

Query: 401 LPH--NDILPALMLSNDLPAHLKRCFSFCAIFPKDYPFRKEQVIHLWIANGLVLP-VKDE 457
 +P +D+L AL SY++LP LK CF+FCA+F K Y FRK+ +IH+WIA L+ + +
 Sbjct: 393 MPPAASDVLSALRRSYDNLPPQLKLCFAFCALFTKGYRFRKDTLIHMWIAQNLIQSTESK 452

Query: 458 INQDLGNQYFLELRSLFEKVPNP SKRNIEELFLMHDLVNDLAQLASSKLCIRLEESQG 517
 ++D+ + F +L R F R ++M+D V+DLA+ S R +E
 Sbjct: 453 RSEDMAEECFDDLVCRRFF-----RYSWGNVYMNDSVHDLARWVSLDEYFRADEDS 504

Query: 518 SHMLEQCRHLSYSIGFNGEFKKLTPLYK-----LEQLRTLLPI-RIEFRLHNLS 565
 H+ + RHLS+ +++T + + L LRTLL + + EFR ++L

Elast Result

Sbjct: 505 LHSKPIRHLWCSS-----ERITNVLEDNNTGGDAVNPLSSSLRTLLFLGQSEFRSYHLL 558

Query: 566 KRVLHNILPTLRSLRALSFSQYKIKELPNDLFTKLKLLRFLDISRTWITKLPDSICGLYN 625
R+ L +R L FS I+ LP+ + LK LR+L +S T I +LP+S+ L

Sbjct: 559 DRMFR----MLSRIRVLDFSNCVIRNLPSSV-GNLKHLRYLGLSNTRIQLRPESVTRLCL 613

Query: 626 LETLLSSCADLEELPLQMEKLINLRHLDVSNTRRLKMPHLHLSRLKSLQVLVGPKFFVD- 684
L+TLLL C +L LP M +L+ LR L +N + + RL LQ L + VD

Sbjct: 614 LQTLLEGC-ELCRLPRSMSRLVKLRQLK-ANPDVIADIAKVGRLELQELKA--YNVDK 669

Query: 685 --GWRMEDLGEAQNHLGSLSVVKLENVDRREAVKAKMREKNHVEQLSLEWSESSIADNS 742
G + +L LHG LS+ L+NV RE+ KA++ EK ++ L L W++ A

Sbjct: 670 KKGHGIAELSAMNQLHGDLSIRNLQNVKTRSRKARLDEKQKLKLLDLRWADGRGAGEC 729

Query: 743 QTESDILDELCPHKNIKKVEISGYRGTFNFPNWVADPLFLKLVNLSLRNCKDCYSLPALGQ 802
+ +L L PH N++++ I Y GT+ P+W+ D + + LR+C LP LGQ

Sbjct: 730 DRDRKVLKGLRPHPNLRELSIKYGGTSSPSWMTDQYLPNMETIRLRSCARLTLPCLGQ 789

Query: 803 LPCLKFLSVKGMHGIRVVTEEFYGRLSKKPFNSLEKLEFEDMTEWKQWH--ALGIGFEP 860
L L+ L + GM +R + +FYG F LE L M ++W FP

Sbjct: 790 LHILRHLHIDGMSQVRQINLQFYG-TGEVSGFPLELLNIRRMPSLEEWSEPRRNCCYFP 848

Query: 861 TLENLSIKNCPELSLEIPIQFSSSKRLEVSDCPVVFDDAQLFRSQLEAMQIEEIDICDC 920
L L I++CP L +P +L+ L +S +V + + + +C

Sbjct: 849 RLHKLLIEDCPRLR-NLPSLPPTLEELRISRTGLVDLPGFHNGDVTNVSLSLHVSEC 907

Query: 921 NSVTSFPFSILPTTLKRIQISRCPKLKLEAPVGEMFVEYLRVNDGCVDDISPEFLPTA- 979
+ S +L L ++ + DC ++ + E TA

Sbjct: 908 RELRSLSEGLLQHNVLALKTA-----AFTDCDSLEFLPAEGFRTAI 948

Query: 980 --RQLSIENCQNVTRFLIPTATETLRISNC----ENVEKLSVACGGAAQMTSLNIWGXXX 1033
L + NC FL+P++ E L++ C N + LS ++ L+I

Sbjct: 949 SLESLIMITNCPPLCSFLLPSSLEHLKLQPCLYPNNEDSLSTCFENLTSLSFLLDI----- 1003

Query: 1034 XXXXXXXXXXXXXXXXXXXDCPEIEGELPFNLEILRIIYCKKLVNGRKEWHLQRLTELWIDH 1093
DCP + P L L + LVN QRL +

Sbjct: 1004 -----KDCPNLSSFPPLCQLSALQHLSLVN-----CQRLQSI----- 1037

Query: 1094 DGSDIEDIEHWELPCSIQRLTIKNLKTLSQHL-----KSLTSLQYLCI-----EG 1138
++ S++ LTI+N L+ H S T L + +G

Sbjct: 1038 -----GFQALTSLESLTIONCPRLTMSHSLVEVMNSSDTGLAFNITRWMRRRTGDDG 1089

Query: 1139 YL---XXXXXXXXXXXXHLSLQTLQIWN-----FLNXXXXXXXXXXXXXXXXXIDDCP 1190
+ HLT LQ L+I I DCP

Sbjct: 1090 LMLRHRAQNDSFFGGLLQHLTFLQFLKICQCPQLVTFTGEEEEKWRNLTSLQILHIVDCP 1149

Query: 1191 NLQSLFESALPS--SLSQLFIQDCPNLQSLPFGMPSSLSKLSIFNCPLLTPLLEFDKGE 1248
NL+ L + L S SLS L+I CP + + P G+ SL+ L I CP L + G+

Sbjct: 1150 NLEVL-PANLQSLCSLSTLYIVRCPRIHAFPPGGVSMHLVIHECPQLCQRCPPGGD 1208

Query: 1249 YWPQIAHIPII 1259
WP IA++P I

Sbjct: 1209 DWPLIANVPRI 1219

CPU time: 0.08 user secs. 0.02 sys. secs 0.10 total secs.

Lambda K H
0.320 0.137 0.408

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 10,906

Blast Result . ;

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Number of extensions: 7195
Number of successful extensions: 35
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 1266
Length of database: 765,046,178
Length adjustment: 142
Effective length of query: 1124
Effective length of database: 765,046,036
Effective search space: 859911744464
Effective search space used: 859911744464
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.0001 wordsize: 3 Filter ☒ Align

Prior Art

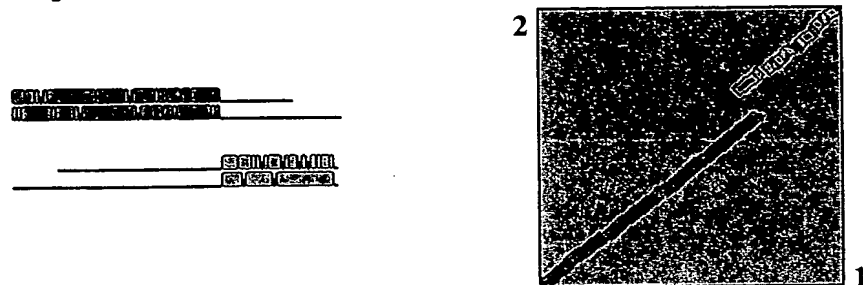
Claimed

D4

828 18/10/2

Sequence 1 lcl|seq_1 Length 1220 (1 .. 1220)

Sequence 2 lcl|seq_2 Length 1441 (1 .. 1441)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 401 bits (1031), Expect = e-109

Identities = 300/911 (32%), Positives = 463/911 (49%), Gaps = 69/911 (7%)

Query: 1 MEIGLAIGGAFLLSSALNVLFDR LAPNGDLLNMFRKHTDDVELFEKLG DILLSLQIVLSDA 60
M L IGG F S + L D+ A N + + R+ +L +L LL + +L A
Sbjct: 1 MSTALVIGGWFAQSFIQTLLDK-ASNCAIQQLARRRGLHDDL-RLR TSLRLRIHA ILDKA 58

Query: 61 ENK-KASNQFVSQWLHKLQTA VDAAENLIEQVNYEALRLKVETSNQQVSDL---NLCLSD 116
E + N + + + +L+ A AE+L+E++ Y+A + KVE Q+SDL +L +
Sbjct: 59 ETRWNHKNTSLVELVRQLKDAAYDAEDLLEELEYQAAKQKVEHRGDQISDLFSFSLSTAS 118

Query: 117 DFF-----LNIKKKL----EDTIKKLEVLEKQIGRLGLKEHFISTKQET RTPST 161
++ I+ KL D + +++L G G + + ++ET +
Sbjct: 119 EWL GADGDDAGTRLREIQGKLCNIAADMM DVMLLAPDDG--GRQFDWKVVRRET----S 172

Query: 162 SLVDDSGIFGRKNEIENLVGRLLSMDTKRKNLAVVPIVGMGMGKTTLAKAVYNDERVQK 221
S + ++ +FGR E E +V LL + + +V+P+VG+GG+GKTTLA+ VYND RV
Sbjct: 173 SFLTETVVFGRDQEREKVVELLLDSGSGNSSFSVLPLVGIGGVGKTTLAQLVYNDNRVGN 232

Query: 222 HFGLTAWFCVSEAYDAFRITKGLLQEIGSTDLKADDNLNQLQVVKL KADDNLNQLQVVKLKE 281
+F L W CVS+ ++ R+TK +++ +T ++ D LN L+ LQ LKE
Sbjct: 233 YFHLKVWVCVSDNFNVKRLTKEIIES--ATKVEQSDKLN-----LDTLQQILKE 279

Query: 282 KLNGKRFLVLVDDVWNDNYPEWDDLRLNLFQGDIGSKIIVTTRKESVALMMDS-GAIYMG 340
K+ +RFL+VLDDVW++N +W+ L GSK+IVTTR +A ++ + I +
Sbjct: 280 KIASERFLLVLDDVWSEN RDDWERLCAPLRFAARGSKVIVTTRDTKIASIIGTMKEISLD 339

Query: 341 ILSSEDSWALFKRHSLEHKDPKEHPEFEEVGKQIADXXXXXXXXXXXXXXXXXRSKSEVDE 400
L + W LFK+ + +P+EH E E +G++IA R +
Sbjct: 340 GLQDDAYWELFKKCAFGSVNPQEHLELEVIGRKIAGKLKGSPLAAKTLGSLRLRLDVSQEH 399

Query: 401 WRNILRSEIWELPSCSNGILPALMLSYNLPAHLKQCFAYCAIYPKDYQFRKEQVIHLWI 460
WR I+ SE+W+LP N ILP L LSY LP HL+QCFA+CA++ KDY F K ++I WI
Sbjct: 400 WRTIMESEVWQLPQAENEILPVLWLSYQHLPGHLRQCFAFCAVFKDYLFYKHELIQTWI 459

Query: 461 ANGLV-HQFHS-----GNQYFIELRSRSLFEMASEPSE RDVEEFLMHDLVNDLAQIASSN 514
A G + HQ + G+ YF EL +RS F+ R ++MHD L++DLAQ S

Sbjct: 460 AEGFIAHQGNKRMEDVGSSYFHELVNRSFFQ-----ESRWRGRYVMHDLIHDLAQFISVG 514

Query: 515 HCIRLEDNKGSHMLEQCRHMSYSIGQDGEFEKLKSLFKSEQLRTLPLID--IQFHYSKKL 572
C R++D+K RH+S ++ E KL +LRTL+ + Q+ Y K+

Sbjct: 515 ECHRIDDDKSKETPSTTRHLSVAL---TEQMKLVDFSGYNKLRTLMINNQPNQYPYMTKV 571

Query: 573 SKRVL-HNILPTLRSLRALSLSHYQIEVLPNDLFIKLKLLRFLDLS-ETSITKLPDSIFV 630
+ +L H++ L+ + L L ++ LP D+ L LR+LD+S I +LP+S+

Sbjct: 572 NSCLLPHSFLKRLKRIHVVLVQKCGMKELP-DIIGDLIQLRYLDISYNACIQRLPESLCD 630

Query: 631 LYNXXXXXXXXXXXXXXXXXXXXQMEKLINLRHLDISNTRRLKMPHLHLSRLKSLQVLVGAKFL 690
LYN M KLINLR L + + K+ + +L SLQ L K L

Sbjct: 631 LYNLQALRLWGCQLRSFPQG-MSKLINLRQLRVEDEIISKI-YEVGKLISLQELSAFKVL 688

Query: 691 VG-GWRMEYLGEAHNLYGSLSSILELENVVDRREAVKAKMREKNHVEQLSLEWSE---SIS 746
G ++ L L +L I LENV + EA KAK+ K ++E L LEW+ S

Sbjct: 689 NNHGKLAELSGLTQLRSTLRITNLENVGSKEEASKAKLHRKQYLEALELEWAAGQVSSL 748

Query: 747 ADNSQTERDILDELPHKNIKAVEITGYRGTFNPNWVADPLFVKLVHLYLRNCKDCYSLP 806
++L L+PH +K++ I GY G P+W+ + L L L NC L

Sbjct: 749 EHLLVSEEVLGLQPHHFLKSLTIRGYSGATVPSWLDVKMLPNLGLTKLENCNTRLEGLS 808

Query: 807 ALGQLPCLEFLSIRGMHGIRVVTEEFYGRLLSSKKPFNSLVKLRFEDMPEWKQWHTLGIGE 866
+GQLP L+ L ++ M ++ ++ E G SK F L +L EDMP K++ L +

Sbjct: 809 YIGQLPHLKVLMKMPVVKQMSHELGCCTKSKL-FPRLEELVLEDMPTLKEFPNL--AQ 865

Query: 867 FPTLEKLSIKN 877
P L+ + +KN

Sbjct: 866 LPCLKIIHMKN 876

Score = 71.6 bits (174), Expect = 2e-10
Identities = 110/463 (23%), Positives = 172/463 (36%), Gaps = 88/463 (19%)

Query: 788 FVKLVHLYLRNCKDCYSLPALGQLPCLEFLSIRGMHGIRVVTEEFYGRLLSSKKPFNSLVK 847
F +L L ++ L +L +LPCL+ I+G+ ++ + ++ F L

Sbjct: 997 FPRLEELEIKGMLTFEELHSLEKLPLCKVFRIKGLPAVKKIGHGLFDSTCQRECFPRLED 1056

Query: 848 LRFEDMPEWKQWHTLGIGE-FPTLEKLSIKNCPELSLEIPIQFSSLKRLDICDCKSVTSF 906
L DMP W++W E F L +L I+ CP+L +PI

Sbjct: 1057 LVLSDMPAWEWSWAEREELFSLCLRLKIEQCPLKCLLP----- 1097

Query: 907 PFSILPTTLKRIKISGCPKLKLEAPVGE---MFVEYLSVIDC---GCVDDISPEFLPT 958
P S++ L ++ ++G P L G + L +I C + + LP

Sbjct: 1098 PHSLIKLELWQVGLTGLPGLCKGIGGSSTRTASLLHIIKCPNLRNLGEGLLSNHLP 1157

Query: 959 ARQLSIENCHN-----VTRFLIPTATESLHIRNCEKL-SMA-CGGAAQLTSLNIWGXXXX 1011
+ I C V RF T E+L IRNC KL SM C L I

Sbjct: 1158 INAIRIWECAELLWLPVKRFREFTTLENLSIRNCPKLMSMTQCEENDLLPPLIKALELG 1217

Query: 1012 XXXXXXXXXXXXXXXTYCPEIEGELP-----FNLQILDIRYCKKLVNGRKE--WHLQRL 1063
C + LP +L L I C +V+ +E HL+ L

Sbjct: 1218 D-----CGNLGKSLPGCLHNLSSLTQLAISNCPYMVSLPREVMLHLKEL 1261

Query: 1064 TELWIKHDGSDEHIEHWELPSSIQRFLIFNL-----KTLSSQHL----- 1102
+ I++ IE ++ S++RL I + LS L

Sbjct: 1262 GTVRIENC DGLSGIEGLQVLKSLKRLAIIGCPRLLLNEGDEQGEVLSLLELSVDKTALLK 1321

Query: 1103 -----KSLTSLQFLRIVGNXXXXXXXXXXXXXH-LTSLQTLQIWNFLNXXXX-XXXXXX 1155
+L + LRI+ + H LT+L+ L+ + N

Sbjct: 1322 LSLIKNTLPFIHSLRIIWSPPQKVMFDLEEQLVHSLTALRRLEFFRCKNLQSLPTELHTL 1381

Query: 1156 XXXXXXIISNCPNLQSLPLKGMPSLSTLSISKC-PLLTPLLE 1197
++S+CP +QSLP KG+P+ L+ L C P+LT LE

Sbjct: 1382 PSLHALVVSDCPQIQSLPEKGLPTLLTDLGFDHCHPVLTAALE 1424

CPU time: 0.16 user secs. 0.00 sys. secs 0.16 total secs.

Lambda	K	H
0.320	0.137	0.406

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 12,261

Number of extensions: 8166

Number of successful extensions: 28

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's gapped: 3

Number of HSP's successfully gapped: 2

Number of extra gapped extensions for HSPs above 10.0: 0

Length of query: 1220

Length of database: 765,046,178

Length adjustment: 142

Effective length of query: 1078

Effective length of database: 765,046,036

Effective search space: 824719626808

Effective search space used: 824719626808

Neighboring words threshold: 9

Window for multiple hits: 0

X1: 16 (7.4 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.8 bits)

S2: 83 (36.6 bits)



Blast 2 Sequences results

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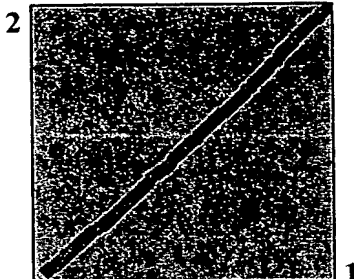
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ AlignPrior Art
D4Claimed
SAD:4

Sequence 1 lc|seq_1 Length 1220 (1 .. 1220)

Sequence 2 lc|seq_2 Length 1232 (1 .. 1232)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 399 bits (1024), Expect = e-109

Identities = 352/1233 (28%), Positives = 552/1233 (44%), Gaps = 129/1233 (10%)

Query: 50 LLSLQIVLSDAENKKASNQFVSQWLHKLQTAVDAAENLIEQVNYEALRLKVETSNQQVSD 109
LL +L +A+ ++ +++ + WL +L+ A+++++ A+RLKV S +
Sbjct: 47 LLRTHSLLEEAKARRMTDKSLVLWLMELKEWAYDADDILDEYEAAAIRLKVTRSTFKR-- 104

Query: 110 LNLCLSDFFLNLIK--KKLEDTIKKLE--VLEKQIGRLGLKEHFISTKQETRTPSTSLVD 165
L D +N+ K+ D K+L LE+++ LG E R +TSL+
Sbjct: 105 ----LIDHVI INVPLAHKVADIRKRLNGVTLERELN-LGALEGSQPLDSTKRGVTTSLLT 159

Query: 166 DSGIFGRKNEIENLVGRLLSMDTKRKNLAVVPIVGMGGMGKTTLAKAVYNDERVQKHFGFL 225
+S I GR + ENL+ LL + + VVPIVG+GG GKTTL++ ++ND+RV++HF L
Sbjct: 160 ESCIVGRAQDKENLIRLLL--EPSDGA VVPIVGLGGAGKTTLSQLIFNDKRVEEHFPL 217

Query: 226 TAWFCVSEAYDAFRITKGLLQEIGSTDLDKADDNLNQLQVVKLADDNLNQLQVVKLKEKLNG 285
W CVS+ +D RIT+ + T+ + L NLN LQV LKE++ G
Sbjct: 218 RMWVCVSDDFDVKRITREI-----TEYATNGRFMDLT-----NLNMLQVNLKEEIRG 264

Query: 286 KRFLVVLDDVWVNDNYPEWDDLRLNLFQGDIGSKIIVTTRKESVALMMDSGAIY-MGILSS 344
FL+VLDDVWN++ +W+ L G GS +IVTT+ + VA + + Y + L+
Sbjct: 265 TTFLVVLDDVWVNDPVKWESLLAPLDAGGRGSVVIVTTQSKKVADVTGTMEPYVLEELTE 324

Query: 345 EDSWALFKRHSL-EHKDPKEHPEFEEVGKQIADXXXXXXXXXXXXXXXXXRSKSEVDEWRN 403
+DSW+L + HS E +P EE+G++IA RSK WR
Sbjct: 325 DDSWSLIESHSFREASCSSTNPRMEEIGRKIAKKISGLPYGATAMGRYLRSKHGESSWRE 384

Query: 404 ILRSEIWELPSCSNGILPALMLSYNLPAHLKQCFAYCAIYPKDYQFRKEQVIHLWIANG 463
+L +E WE+P ++ +L AL SY++LP LK CFA+CA++ K Y+FRK+ +IH+WIA
Sbjct: 385 VLETETWEMPPAASDVLSALRRSYDNLPPQLKLCFAFCALFTKGYRFRKDTLIHMWIAQN 444

Query: 464 LVHQFHS-----GNQYFIELRSRSLFEMASEPSESDVEEFLMHDLVNDLAQIASSNHCI 517
L+ S + F +L R F + ++M+D V+DLA+ S +
Sbjct: 445 LIQSTESKRSEDMAEECFDDLVCRRFFFRYSWG-----NYVMNDSVHDLARWVSLDEYF 497

Query: 518 RLEDNKGSHMLEQCRHMSYSIGQDGEFEKLKSLFKSEQ-----LRTLPIIDIQF 566
R +++ H+ + RH+S+ E++ ++ + LRTL +

Blast Result

```

Sbjct: 498  RADEDSPLHISKPIRHLSWCS-----ERITNVLEDNNTGGDAVNPLSSLRTLLFLG--- 548

Query: 567  HYSKKLSKRVLHNILPTLRSLRALSLSHYQIEVLPNDLFIKLKLRLFLDLSETSITKLPD 626
          S+  S  +L  +  L  +R L  S+  I  LP+  +  LK LR+L LS T I +LP+
Sbjct: 549  -QSEFRSYHLLDRMFRMLSRIRVLDFSNCVIRNLPSSVG-NLKHLRYLGLSNTRIQLRPE 606

Query: 627  SIFVLYNXXXXXXXXXXXXXXXXXXXXQMEKLINLRHL-----DISNTRRLKMPHLHSRL 678
          S+  L                               M +L+ LR L           DI+  RL  + L  L
Sbjct: 607  SVTRLC-LLQTLTLLGCELCRLPRSMSRLVKLRQLKANPDVIADIAKVGR---IELQEL 662

Query: 679  KSLQVLVGAKFLVGGWRMEYLGEAHNLYGSLSILELENVVDRREAVKAKMREKNHVEQLS 738
          K+  V           G  +  L  + L+G LSI  L+NV  RE+  KA++  EK  ++  L
Sbjct: 663  KAYNVDKKK-----GHGIAELSAMNQLHGDLISIRNLQNVEKTRESRKARLDEKQKLKLLD 717

Query: 739  LEWSESIADNSQTERDILDELPHKNIKAVEITGYRGTFNPNWVADPLFVKLVHLYLRN 798
          L W++  A           +R +L  LRPH N++  +  I  Y GT+  P+W+  D           +  +  LR+
Sbjct: 718  LRWADGRGAGECDRDRKVLKGLRPHPNLRELSIKYYGGTSSPSWMTDQYLPNMETIRLRS 777

Query: 799  CKDCYSLPALGQLPCLEFLSIRGMHGIRVVTEEFYGRLLSSKKPFNSLVKLRFEDMPEWKQ 858
          C           LP LGQL  L  L  I GM  +R  +  +FYG           F  L  L  MP  ++
Sbjct: 778  CARLTCLPCLGQLHLRHLHDGMSQVRQINLQFYG-TGEVSGFPLELLNIRRMPSLEE 836

Query: 859  WH--TLGIGEFPTLEKLSIKNCPCL-----SLEIPIQFSSLKRLDICCKSVTSFPFSILP 912
          W           FP L KL I++CP L           SL  ++  + R  +  D
Sbjct: 837  WSEPRRCCYFPRHLKLLIEDCPRLRNLPSPPTLEELRISRTGLVDLPGFHNGDVTTN 896

Query: 913  TTLKRIKISGCPKLEAPVGEMFVEYLSVIDCGCVDDISPEFLP-----TARQLSI 964
          +L  +  +S C +L+           G  +  +++           D  S EFLP           +  L  +
Sbjct: 897  VSLSSLHVSECRELR-SLSEGLLQHNLVALKTAaftDCDSLEFLPAEGFRTAISLESIM 955

Query: 965  ENCHNVTRFLIPTATESLHIRNC-----EKLSMACGGAAQLTSLNIWGXXXXXXX--- 1014
          NC           FL+P++  E L  ++  C           + LS           L+  L+I
Sbjct: 956  TNCPLPCSFLPSSLEHLKLQPCLYPNNNEDSLSTCFENLTSLSFLLDIKDCPNLSSFPFG 1015

Query: 1015 -XXXXXXXXXXXXXTYCPEIEG---ELPFNLQILDIRYCKKL-----VNGRKEWHLQR 1062
          C  ++  +  +L+  L I+  C +L           VN  +  L
Sbjct: 1016 PLCQLSALQHLSLVNCQRLQSIGFQALTSLESLTIONCPRLTMSHSLVEVNNSSDTGLAF 1075

Query: 1063 LTELWIKHDGSDEHIEHWELPSSIQRLFIFNLKTLSSQHLKSLTSLQFLRIVG-NXXXXX 1121
          W++  D+  +  L  Q  F           L+  LT LQFL+I
Sbjct: 1076 NITRWMRRRTGDDGL---MLRHRAQNDSFF-----GGLLQHLTFLQFLKICQCPQLVTF 1126

Query: 1122 XXXXXXXXXXXHLSLQTLQIWNFLNXXXXXXXXXXXXXXXXXXXXI-ISNCPNLQSLPLKGMPS 1180
          +LTSLQ L I  +  N           + I  CP  +  +  P  G+  S
Sbjct: 1127 TGEERKWRNLTSLQILHIVDCPNLEVL PANLQSLCSLSTLYIVRCPRIHAFPPGGVSM 1186

Query: 1181 LSTLSISKCPLLTPLLEFDKGEYWTEIAHIPTI 1213
          L+  L I +CP L  +  G+  W  IA++P I
Sbjct: 1187 LAHLVIHECPQLCQRCDPPGGDDWPLIANVPRI 1219

```

CPU time: 0.09 user secs. 0.01 sys. secs 0.10 total secs.

Lambda	K	H
0.320	0.137	0.406

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Sequences: 1
 Number of Hits to DB: 9918
 Number of extensions: 6581
 Number of successful extensions: 26
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1

Blast Result

Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 1220
Length of database: 765,046,178
Length adjustment: 142
Effective length of query: 1078
Effective length of database: 765,046,036
Effective search space: 824719626808
Effective search space used: 824719626808
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 gap open: 11 gap extension: 1

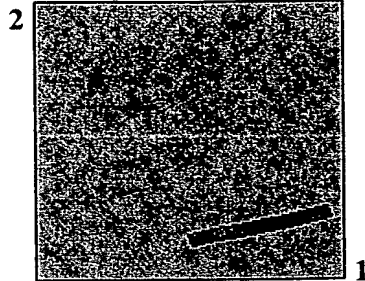
x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ Align

D5

Claimed
D5 100:2

Sequence 1 lcl|seq_1 Length 318 (1 .. 318)

Sequence 2 lcl|seq_2 Length 1441 (1 .. 1441)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 34.3 bits (77), Expect = 6.9

Identities = 31/149 (20%), Positives = 66/149 (43%), Gaps = 6/149 (4%)

Query: 159 SIIGVHGLGGVGXXXXXXXXXXXXXXXXXXRDYHVVIMIEVANSETLNVVDMQK-IIANRLA 217
S++ + G+GGVG +H+ + + V S+ NV + K II +
Sbjct: 205 SVLPLVGIGGVGKTTLAQLVYNDNRVGNV-FHLKVWVCV--SDNFNVKRLTKEIIESATK 261

Query: 218 LPWNESETERERSTYLRRALRRKKFVVLDDVW--KKFQLADVGIPTPSSDKGCKLILAS 275
+ ++ L+ + ++F+++LDDVW + + P + +G K+I+ +
Sbjct: 262 VEQSDKLNLDLTLQILKEKIASERFLLVLDDVWSENRRDWERLCAPLRFAARGSKVIVTT 321

Query: 276 RSNQVCVEMGDKEPMEMPCLGDNESLRLF 304
R ++ +G + + + L D+ LF
Sbjct: 322 RDTKIASIIGTMKEISLDGLQDDAYWELF 350

CPU time: 0.04 user secs. 0.00 sys. secs 0.04 total secs.

Lambda	K	H
0.319	0.135	0.400

Gapped Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 2615

Number of extensions: 1870

Number of successful extensions: 2

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 0

Number of HSP's gapped: 2

Number of HSP's successfully gapped: 1

Number of extra gapped extensions for HSPs above 10.0: 1

Length of query: 318

Blast Result

Length of database: 765,046,178
Length adjustment: 130
Effective length of query: 188
Effective length of database: 765,046,048
Effective search space: 143828657024
Effective search space used: 143828657024
Neighboring words threshold: 9
Window for multiple hits: 0
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 76 (33.9 bits)



Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.10 [Oct-19-2004]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.0001 wordsize: 3 Filter ☒ Align

Prior Art

Claimed

Sequence 1 lcl|seq_1 Length 318

DS

SEQ ID NO: 4

Sequence 2 lcl|seq_2 Length 1232

No significant similarity was found

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